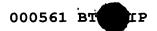


Patent claims

- 1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the mikE17 gene, chosen from the group consisting of
 - a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,
- 10 b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,
- c) polynucleotide which is complementary to the polynucleotides of a or b), and
 - d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),
- the polypeptide preferably having the activity of the transcription regulator MikE17.
 - 2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.
- 3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
 - 4. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.
 - 5. A DNA as claimed in claim 2 which is capable of replication, comprising
- 30 (i) the nucleotide sequence shown in SEQ ID No. 1, or



- (ii) at least one sequence which corresponds to
 sequence (i) within the range of the
 degeneration of the genetic code, or
- (iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and optionally
 - (iv) sense mutations of neutral function in (i).
 - 6. A DNA as claimed in claim 5 which is capable of replication,
- the hybridization is carried out under a stringency corresponding to at most 2x SSC.
- 7. A polynucleotide sequence as claimed in claim 1, which codes for a polypeptide which comprises the amino acid sequences shown in SEQ ID No. 2.
 - 8. A coryneform bacterium in which the mikE17 gene is attenuated, in particular eliminated.
 - 9. The vector pCR2.1mikE17int,
- 9.1 the restriction map of which is reproduced in figure 1 and which
 - 9.2 is deposited in the E.coli strain

 Top10/pCR2.1mixEl7int under no. 14143 at the

 Deutsche Sammlung für Mikroorganismen und

 Zellkulturen (DSNZ = German Collection of

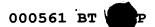
 Microorganisms and Cell Cultures, Braunschweig)

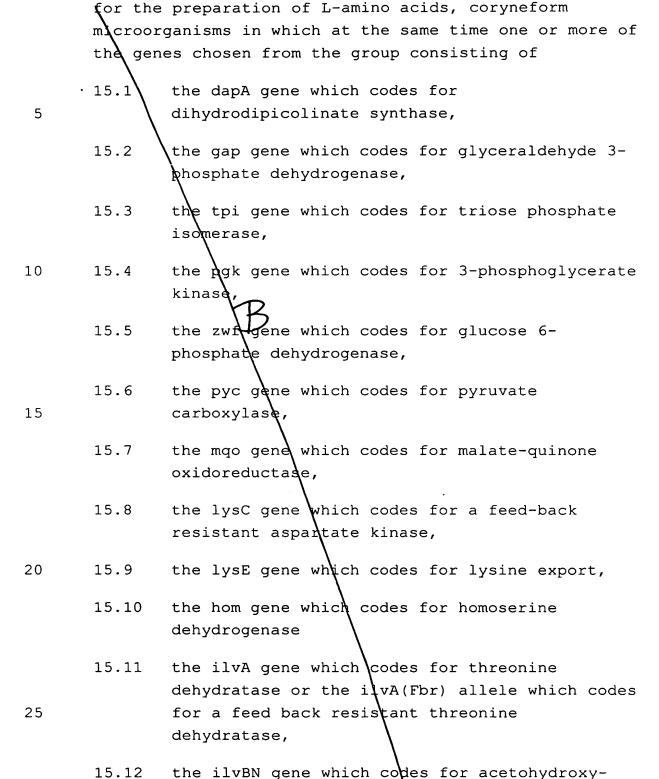
 in accordance with the Budapest Treaty.
 - 10. A process for the fermentative preparation of L-amino acids, in particular L-lysine, which comprises
- 30 carrying out the following steps:

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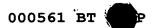
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- a) fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the mikE17 gene or nucleotide sequences which code for it are attenuated, in particular eliminated,
- 5 b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and
 - c) isolation of the L-amino acid, the biomass and/or constituents of the fermentation broth optionally remaining in their entire amount or in portions in the product obtained in this way.
 - 11. A process as claimed in claim 10,
 wherein
 bacteria in which further genes of the biosynthesis
 pathway of the desired L-amino acid are additionally
 enhanced are employed.
- 12. A process as claimed in claim 10,
 wherein
 bacteria in which the metabolic pathways which reduce
 the formation of the desired L-amino acid are at least
 partly eliminated are employed.
- 13. A process as claimed in claim 10,
 wherein
 the expression of the polynucleotide(s) which code(s)
 for the mikE17 gene is attenuated, in particular
 eliminated.
 - 14. A process as claimed in claim 10, wherein the regulatory properties of the polypeptide (enzyme protein) for which the polynucleotide mikE17 codes are reduced.
 - 15. A process as claimed in claim 10, wherein





acid synthase,



- 15.13 the ilvD gene which codes for dihydroxy-acid dehydratase,
- 15. 4 the zwal gene which codes for the Zwal protein is on are enhanced or over-expressed are fermented.
- 5 16. A process as claimed in claim 10,
 wherein
 for the preparation of L-amino acids, coryneform
 microorganisms in which at the same time one or more of
 the genes chosen from the group consisting of
- 10 16.1 the pck gene which codes for phosphoenol pyrtwate carboxykinase,
 - 16.2 the pgi gene which codes for glucose 6phosphate isomerase,
 - 16.3 the pox gene which codes for pyruvate oxidase
- 15 16.4 the zwa2 gene which codes for the Zwa2 protein is or are attenuated, in particular eliminated, are fermented.
- 17. A coryneform bacterium which contains a vector which carries parts of the polynucleotide as claimed in claim 1, but at least 15 successive nucleotides of the sequence claimed.
 - 18. A process as claimed in one or more of the preceding claims, wherein
- 25 microorganisms of the species Corynebacterium glutamicum are employed.
 - 19. A process for discovering RNA cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for the transcription regulator MikE17 or

have a high similarity with the sequence of the mikE17 gene, which comprises employing the polynucleotide comprising the polynucleotide sequences as claimed in claims 1, 2, 3 or 4 as hybridization probes.

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